REMARKS

Applicants are submitting copies of Figures 2, 8 and 13 with proposed revisions marked. The revisions to Figure 2 merely correct errors in the numbering of the amino acid sequence; the revisions to Figures 8 and 13 merely insert the identifications of the corresponding residues of SEQ ID NO:3. None of these revisions present new matter. Approval of these revisions to Figures 2, 8 and 13, is respectfully requested.

Applicants have added into the present specification a new paper copy Sequence Listing section according to 37 C.F.R. §1.821(c) as new pages 1-4. Furthermore, attached hereto is a 3 1/2" disk containing the "Sequence Listing" in computer readable form in accordance with 37 C.F.R. §1.821(e).

Applicants have amended the specification to insert SEQ ID Nos, as supported in the present specification.

The following statement is provided to meet the requirements of 37 C.F.R. §1.821(f) and 1.821(g).

I hereby state, in accordance with 37 C.F.R. §1.821(f), that the content of the attached paper and computer readable copies of the sequence listing are believed to be the same.

I hereby also state, in accordance with 37 C.F.R. §1.821(g), that the submission is not believed to include new matter.

Under U.S. rules, each sequence must be classified in <213> as an "Artificial Sequence", a sequence of "Unknown"

origin, or a sequence originating in a particular organism, identified by its scientific name.

Neither the rules nor the MPEP clarify the nature of the relationship which must exist between a listed sequence and an organism for that organism to be identified as the origin of the sequence under <213>.

Hence, counsel may choose to identify a listed sequence as associated with a particular organism even though that sequence does not occur in nature by itself in that organism (it may be, e.g., an epitopic fragment of a naturally occurring protein, or a cDNA of a naturally occurring mRNA, or even a substitution mutant of a naturally occurring sequence). Hence, the identification of an organism in <213> should not be construed as an admission that the sequence *per se* occurs in nature in said organism.

Similarly, designation of a sequence as "artificial" should not be construed as a representation that the sequence has no association with any organism. For example, a primer or probe may be designated as "artificial" even though it is necessarily complementary to some target sequence, which may occur in nature. Or an "artificial" sequence may be a substitution mutant of a natural sequence, or a chimera of two or more natural sequences, or a cDNA (i.e., intron-free sequence) corresponding to an intron-containing gene, or otherwise a fragment of a natural sequence.

The Examiner should be able to judge the relationship of the enumerated sequences to natural sequences by giving full consideration to the specification, the art

cited therein, any further art cited in an IDS, and the results of his or her sequence search against a database containing known natural sequences.

Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment. The attached page is captioned "Version with markings to show changes made".

Applicants submit that the present application contains patentable subject matter and therefore urge the examiner to pass the case to issuance.

If the examiner has any questions or comments concerning the above described application, the examiner is urged to contact the undersigned at the phone number below.

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the specification:

The paragraphs numbered 32 and 33 of page 12 have been amended as follows:

[0032.] Figure 1 compares the amino acid sequence of SP22 (SEQ ID NO:3) and DJ-1 (SEQ ID NO:1), and illustrates the four peptides identified following Edman degradation that were used to identify the homology with DJ1 and correct sequences of these peptides as they exist in SP22.

[0033.] Figure 2 shows ~~SEQ ID NO:3 which compares~~ the nucleotide (SEQ ID NOs:2 and 4) and amino acid (SEQ ID NO:3) sequences of the two SP22 mRNA transcripts, A (SEQ ID NO:2) and B (SEQ ID NO:4). The A transcript is SP22A and is unique to the testis and referred to as SEQ ID NO:2.

The paragraph numbered 39 of page 13 has been amended as follows:

[0039.] Figure 8 is a plot illustrating the immunoreactivity of overlapping 15 mer SP22 peptides with affinity-purified anti-SP22 peptide Ig. Antiserum was affinity-purified and diluted 1:100 prior to use. The two reactive peaks within the 189 amino acid SP22 sequence are: Peptide A (TVAGLAGKDPVQCSR) (residues 34-48 of SEQ ID NO:3) and Peptide B (DGLILTSR) (residues 149-156 of SEQ ID NO:3).

The paragraph numbered 44 of page 15 has been amended as follows:

[0044.] Figure 13 is a plot illustrating the immunoreactivity of overlapping 15 mer PS-22 peptides with affinity-purified anti-recombinant SP22 Ig. Antiserum was affinity-purified and diluted 1:100 prior to use. The three reactive peaks within the 189 amino acid SP22 sequence are: Peptide C (LEEAKTQGPYDV) (residues 58-69 of SEQ ID NO:3), Peptide D (VKEILKEQENRKGLI) (residues 88-102 of SEQ ID NO:3), and Peptide E (GFGCKVTSHPLAKDK) (residues 118-132 of SEQ ID NO:3).

The paragraphs numbered 46 and 47 of page 16 have been amended as follows:

[0046.] Figure 15 shows the nucleotide (SEQ ID NO:2) and amino acid (SEQ ID NO:3) sequences of SP22.

[0047.] Figure 16 shows the longer 5' untranslated regions of SP22A (bases 1-975 of SEQ ID NO:2 and SEQ ID NO:3).